

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/541,598  
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IFWP

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PATENT APPLICATION: US/10/541,598

DATE: 08/10/2006  
TIME: 09:54:22

Input Set : A:\49321-142 SEQ LIST.txt  
Output Set: N:\CRF4\08102006\J541598.raw

3 <110> APPLICANT: Moses, Ashlee  
4 Frueh, Klaus  
5 King, Jeffrey S.  
6 Hicks, James B.  
7 Raggio, Camilo  
8 Nelson, Jay  
10 <120> TITLE OF INVENTION: METHODS OF TREATMENT AND DIAGNOSIS OF KAPOSI'S SARCOMA (KS)

AND

11 KS RELATED DISEASES  
13 <130> FILE REFERENCE: 49321-142  
15 <140> CURRENT APPLICATION NUMBER: US 10/541,598  
16 <141> CURRENT FILING DATE: 2005-07-05  
18 <150> PRIOR APPLICATION NUMBER: US 60/438,343  
19 <151> PRIOR FILING DATE: 2003-01-06  
21 <150> PRIOR APPLICATION NUMBER: US 60/473,246  
22 <151> PRIOR FILING DATE: 2003-05-22  
24 <150> PRIOR APPLICATION NUMBER: PCT US04/00320  
25 <151> PRIOR FILING DATE: 2004-01-06  
27 <160> NUMBER OF SEQ ID NOS: 33  
29 <170> SOFTWARE: PatentIn version 3.3  
31 <210> SEQ ID NO: 1  
32 <211> LENGTH: 2035  
33 <212> TYPE: DNA  
34 <213> ORGANISM: homo sapiens  
37 <220> FEATURE:  
38 <221> NAME/KEY: CDS  
39 <222> LOCATION: (152)..(1240)  
41 <400> SEQUENCE: 1  
42 tgcaagtctg cagccagcag agctcacagt tggcggaaag tgctcagcac taaggagcc 60  
44 agcgcacagc acagccagga aggcgagcga gcccagccag cccagccagc ccagccagcc 120  
46 cggaggtcat ttgattgccc gcctcagaac g atg gat ctg cat ctc ttc gac 172  
47 Met Asp Leu His Leu Phe Asp  
48 1 5  
50 tac tca gag cca ggg aac ttc tcg gac atc agc tgg cca tgc aac agc 220  
51 Tyr Ser Glu Pro Gly Asn Phe Ser Asp Ile Ser Trp Pro Cys Asn Ser  
52 10 15 20  
54 agc gac tgc atc gtg gtg gac acg gtg atg tgt ccc aac atg ccc aac 268  
55 Ser Asp Cys Ile Val Val Asp Thr Val Met Cys Pro Asn Met Pro Asn  
56 25 30 35  
58 aaa agc gtc ctg ctc tac acg ctc tcc ttc att tac att ttc atc ttc 316  
59 Lys Ser Val Leu Leu Tyr Thr Leu Ser Phe Ile Tyr Ile Phe Ile Phe  
60 40 45 50 55  
62 gtc atc ggc atg att gcc aac tcc gtg gtg gtc tgg gtg aat atc cag 364  
63 Val Ile Gly Met Ile Ala Asn Ser Val Val Val Trp Val Asn Ile Gln

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64	60	65	70	
66	gcc aag acc aca gac tat gac acg cac tgc tac atc ttg aac ctg gcc			412
67	Ala Lys Thr Thr Gly Tyr Asp Thr His Cys Tyr Ile Leu Asn Leu Ala			
68	75	80	85	
70	att gcc gac ctg tgg gtt gtc ctc acc atc cca gtc tgg gtg gtc agt			460
71	Ile Ala Asp Leu Trp Val Val Leu Thr Ile Pro Val Trp Val Val Ser			
72	90	95	100	
74	ctc gtg cag cac aac cag tgg ccc atg ggc gag ctc acg tgc aaa gtc			508
75	Leu Val Gln His Asn Gln Trp Pro Met Gly Glu Leu Thr Cys Lys Val			
76	105	110	115	
78	aca cac ctc atc ttc tcc atc aac ctc ttc ggc agc att ttc ttc ctc			556
79	Thr His Leu Ile Phe Ser Ile Asn Leu Phe Gly Ser Ile Phe Phe Leu			
80	120	125	130	135
82	acg tgc atg agc gtg gac cgc tac ctc tcc atc acc tac ttc acc aac			604
83	Thr Cys Met Ser Val Asp Arg Tyr Leu Ser Ile Thr Tyr Phe Thr Asn			
84	140	145	150	
86	acc ccc agc agc agg aag aag atg gta cgc cgt gtc gtc tgc atc ctg			652
87	Thr Pro Ser Ser Arg Lys Lys Met Val Arg Arg Val Val Cys Ile Leu			
88	155	160	165	
90	gtg tgg ctg ctg gcc ttc tgc gtg tct ctg cct gac acc tac tac ctg			700
91	Val Trp Leu Leu Ala Phe Cys Val Ser Leu Pro Asp Thr Tyr Tyr Leu			
92	170	175	180	
94	aag acc gtc acg tct gcg tcc aac aat gag acc tac tgc cgg tcc ttc			748
95	Lys Thr Val Thr Ser Ala Ser Asn Asn Glu Thr Tyr Cys Arg Ser Phe			
96	185	190	195	
98	tac ccc gag cac agc atc aag gag tgg ctg atc ggc atg gag ctg gtc			796
99	Tyr Pro Glu His Ser Ile Lys Glu Trp Leu Ile Gly Met Glu Leu Val			
100	200	205	210	215
102	tcc gtt gtc ttg ggc ttt gcc gtt ccc ttc tcc att atc gct gtc ttc			844
103	Ser Val Val Leu Gly Phe Ala Val Pro Phe Ser Ile Ile Ala Val Phe			
104	220	225	230	
106	tac ttc ctg ctg gcc aga gcc atc tcg gcg tcc agt gac cag gag aag			892
107	Tyr Phe Leu Leu Ala Arg Ala Ile Ser Ala Ser Ser Asp Gln Glu Lys			
108	235	240	245	
110	cac agc agc cgg aag atc atc ttc tcc tac gtg gtg gtc ttc ctt gtc			940
111	His Ser Ser Arg Lys Ile Ile Phe Ser Tyr Val Val Phe Leu Val			
112	250	255	260	
114	tgc tgg ctg ccc tac cac gtg gcg gtg ctg ctg gac atc ttc tcc atc			988
115	Cys Trp Leu Pro Tyr His Val Ala Val Leu Leu Asp Ile Phe Ser Ile			
116	265	270	275	
118	ctg cac tac atc cct ttc acc tgc cgg ctg gag cac gcc ctc ttc acg			1036
119	Leu His Tyr Ile Pro Phe Thr Cys Arg Leu Glu His Ala Leu Phe Thr			
120	280	285	290	295
122	gcc ctg cat gtc aca cag tgc ctg tcg ctg gtg cac tgc tgc gtc aac			1084
123	Ala Leu His Val Thr Gln Cys Leu Ser Leu Val His Cys Cys Val Asn			
124	300	305	310	
126	cct gtc ctc tac agc ttc atc aat cgc aac tac agg tac gag ctg atg			1132
127	Pro Val Leu Tyr Ser Phe Ile Asn Arg Asn Tyr Arg Tyr Glu Leu Met			
128	315	320	325	

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220 Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn  
221 180 185 190  
224 Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp  
225 195 200 205  
228 Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro  
229 210 215 220  
232 Phe Ser Ile Ile Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser  
233 225 230 235 240  
236 Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser  
237 245 250 255  
240 Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val  
241 260 265 270  
244 Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg  
245 275 280 285  
248 Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser  
249 290 295 300  
252 Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg  
253 305 310 315 320  
256 Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala  
257 325 330 335  
260 Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr  
261 340 345 350  
264 Glu Tyr Ser Ala Leu Glu Gln Ser Thr Lys  
265 355 360  
268 <210> SEQ ID NO: 3  
269 <211> LENGTH: 1421  
270 <212> TYPE: DNA  
271 <213> ORGANISM: homo sapiens  
274 <220> FEATURE:  
275 <221> NAME/KEY: CDS  
276 <222> LOCATION: (115)..(1092)  
278 <400> SEQUENCE: 3  
279 ggcgagggag gaggaagaag cggaggaggc ggctcccgcg ctcgcagggc cgtgccacct 60  
281 gcccggccgc ccgctcgctc gctcgccgc cgcggcgcc tgccgaccgc cagc atg 117  
282 Met  
283 1  
285 ctg ccg aga gtg ggc tgc ccc gcg ctg ccg ctg ccg ccg ccg ctg 165  
286 Leu Pro Arg Val Gly Cys Pro Ala Leu Pro Leu Pro Pro Pro Leu  
287 5 10 15  
289 ctg ccg ctg ctg ctg cta ctg ggc gcg agt ggc ggc ggc ggc ggg 213  
290 Leu Pro Leu Leu Leu Leu Gly Ala Ser Gly Gly Gly Gly Gly  
291 20 25 30  
293 gcg cgc gcg gag gtg ctg ttc cgc tgc ccg ccc tgc aca ccc gag cgc 261  
294 Ala Arg Ala Glu Val Leu Phe Arg Cys Pro Pro Cys Thr Pro Glu Arg  
295 35 40 45  
297 ctg gcc gcc tgc ggg ccc ccg ccg gtt gcg ccg ccc gcc gcg gtg gcc 309  
298 Leu Ala Ala Cys Gly Pro Pro Val Ala Pro Pro Ala Ala Val Ala  
299 50 55 60 65  
301 gca gtg gcc gga ggc gcc cgc atg cca tgc gcg gag ctc gtc cgg gag 357

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302	Ala	Val	Ala	Gly	Gly	Ala	Arg	Met	Pro	Cys	Ala	Glu	Leu	Val	Arg	Glu	
303						70					75				80		
305	ccg	ggc	tgc	ggc	tgc	tgc	tcg	gtg	tgc	gcc	cg	ctg	gag	ggc	gag	g	405
306	Pro	Gly	Cys	Gly	Cys	Cys	Ser	Val	Cys	Ala	Arg	Leu	Glu	Gly	Glu	Ala	
307						85				90			95				
309	tgc	ggc	gtc	tac	acc	ccg	cgc	tgc	ggc	cag	ggg	ctg	cgc	tgc	tat	ccc	453
310	Cys	Gly	Val	Tyr	Thr	Pro	Arg	Cys	Gly	Gln	Gly	Leu	Arg	Cys	Tyr	Pro	
311						100				105			110				
313	cac	ccg	ggc	tcc	gag	ctg	ccc	ctg	cag	g	ctg	atg	ggc	gag	ggc		501
314	His	Pro	Gly	Ser	Glu	Leu	Pro	Leu	Gln	Ala	Leu	Val	Met	Gly	Glu	Gly	
315						115				120			125				
317	act	tgt	gag	aag	cgc	cgg	gac	gcc	gag	tat	ggc	gcc	agc	ccg	gag	cag	549
318	Thr	Cys	Glu	Lys	Arg	Arg	Asp	Ala	Glu	Tyr	Gly	Ala	Ser	Pro	Glu	Gln	
319	130					135				140			145				
321	gtt	gca	gac	aat	ggc	gat	gac	cac	tca	gaa	gga	ggc	ctg	gtg	gag	aac	597
322	Val	Ala	Asp	Asn	Gly	Asp	Asp	His	Ser	Glu	Gly	Gly	Leu	Val	Glu	Asn	
323						150				155			160				
325	cac	gtg	gac	agc	acc	atg	aac	atg	ttg	ggc	ggg	gga	ggc	agt	gct	ggc	645
326	His	Val	Asp	Ser	Thr	Met	Asn	Met	Leu	Gly	Gly	Gly	Ser	Ala	Gly		
327						165				170			175				
329	cgg	aag	ccc	ctc	aag	tgc	ggt	atg	aag	gag	ctg	gcc	gtg	ttc	cg	gag	693
330	Arg	Lys	Pro	Leu	Lys	Ser	Gly	Met	Lys	Glu	Leu	Ala	Val	Phe	Arg	Glu	
331						180				185			190				
333	aag	gtc	act	gag	cag	cac	cg	cag	atg	ggc	aag	ggt	ggc	aag	cat	cac	741
334	Lys	Val	Thr	Glu	Gln	His	Arg	Gln	Met	Gly	Lys	Gly	Gly	Lys	His	His	
335						195				200			205				
337	ctt	ggc	ctg	gag	gg	ccc	aag	aag	ctg	cga	cca	ccc	cct	gcc	agg	act	789
338	Leu	Gly	Leu	Glu	Glu	Pro	Lys	Lys	Leu	Arg	Pro	Pro	Pro	Ala	Arg	Thr	
339	210					215				220			225				
341	ccc	tgc	caa	cag	gaa	ctg	gac	cag	gtc	ctg	gag	cg	atc	tcc	acc	atg	837
342	Pro	Cys	Gln	Gln	Glu	Leu	Asp	Gln	Val	Leu	Glu	Arg	Ile	Ser	Thr	Met	
343						230				235			240				
345	cgc	ctt	ccg	gat	gag	cg	gg	cc	cct	ctg	gag	cac	ctc	tac	tcc	ctg	885
346	Arg	Leu	Pro	Asp	Glu	Arg	Gly	Pro	Leu	Glu	His	Leu	Tyr	Ser	Leu	His	
347						245				250			255				
349	atc	ccc	aac	tgt	gac	aag	cat	ggc	ctg	tac	aa	ctc	aaa	cag	tgc	aag	933
350	Ile	Pro	Asn	Cys	Asp	Lys	His	Gly	Leu	Tyr	Asn	Leu	Lys	Gln	Cys	Lys	
351						260				265			270				
353	atg	tct	ctg	aac	ggg	cag	cgt	ggg	gag	tgc	tgg	tgt	gtg	aac	ccc	aac	981
354	Met	Ser	Leu	Asn	Gly	Gln	Arg	Gly	Glu	Cys	Trp	Cys	Val	Asn	Pro	Asn	
355						275				280			285				
357	acc	ggg	aag	ctg	atc	cag	gga	gcc	ccc	acc	atc	cg	ggg	gac	ccc	gag	1029
358	Thr	Gly	Lys	Leu	Ile	Gln	Gly	Ala	Pro	Thr	Ile	Arg	Gly	Asp	Pro	Glu	
359	290					295				300			305				
361	tgt	cat	ctc	tcc	tac	aat	gag	cag	cag	gag	g	ctc	gg	gt	cac	acc	1077
362	Cys	His	Leu	Phe	Tyr	Asn	Glu	Gln	Gln	Glu	Ala	Arg	Gly	Val	His	Thr	
363						310				315			320				
365	cag	cg	atg	cag	tag	accgcagcca	gcccgtgcct	ggcgccccctg	ccccccgccc								1132
366	Gln	Arg	Met	Gln													

**VERIFICATION SUMMARY**

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